

RAW SEQUENCE LISTING

EFS

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Information Center (STIC) no errors detected.

Application Serial Number: 10/561,906
Source: FWP
Date Processed by STIC: 3/28/07

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RAW SEQUENCE LISTING

DATE: 03/28/2007

PATENT APPLICATION: US/10/561,906

TIME: 14:52:59

Input Set : N:\efs\03_28_07\10561906_efs\281642US0XPCTST25.txt

Output Set: N:\CRF4\03282007\J561906.raw

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3 <110> APPLICANT: Patek, Miroslav
4   Elisakova, Veronika
6 <120> TITLE OF INVENTION: FEEDBACK RESISTANT ACETOHYDROXY ACID SYNTHETHASE MUTANTS
8 <130> FILE REFERENCE: 281642US0XPCT
10 <140> CURRENT APPLICATION NUMBER: US 10/561,906
11 <141> CURRENT FILING DATE: 2005-12-21
13 <150> PRIOR APPLICATION NUMBER: PCT/EP04/06157
14 <151> PRIOR FILING DATE: 2004-06-08
16 <150> PRIOR APPLICATION NUMBER: EP 03014640.1
17 <151> PRIOR FILING DATE: 2003-06-26
19 <160> NUMBER OF SEQ ID NOS: 12
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 519
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Synthetic DNA
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(519)
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38 Met Val Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
39 1          5          10          15
41 gac gta gac gat gac ttt tcc cgc gta tca ggt atg ttc acc cga cgc      96
42 Asp Val Asp Asp Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg
43          20          25          30
45 gca ttc aac ctc gtg tcc ctc gtg tct gca aag acc gaa aca cac ggc      144
46 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
47          35          40          45
49 atc aac cgc atc acg gtt gtt gtc gac gcc gac gag ctc aac att gag      192
50 Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
51          50          55          60
53 cag atc aac aag cag ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg      240
54 Gln Ile Asn Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
55 65          70          75          80
57 cga ctt gat gaa gag acc act atc gcc cgc gca atc atg ctg gtt aag      288
58 Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
59          85          90          95
61 gtc tct gcg gac agc acc aac cgt ccg cag atc gtc gac gcc gcg aac      336
62 Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
63          100          105          110

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65 atc ttc cgc gcc cga gtc gtc gac gtg gct cca gac tct gtg gtt att      384
66 Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
67      115      120      125
69 gaa tcc aca ggc acc cca ggc aag ctc cgc gca ctg ctt gac gtg atg      432
70 Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
71      130      135      140
73 gaa caa ttc gaa atc cgc gaa ctg atc caa tcc gga cag att gca ctc      480
74 Glu Gln Phe Glu Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
75 145      150      155      160
77 aac cgc ggt ccg aag acc atg gct ccg gcc aag atc taa      519
78 Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
79      165      170
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83 <211> LENGTH: 172
84 <212> TYPE: PRT
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88 <223> OTHER INFORMATION: Synthetic Construct
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93 1      5      10      15
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97      20      25      30
100 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
101      35      40      45
104 Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
105      50      55      60
108 Gln Ile Asn Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
109 65      70      75      80
112 Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
113      85      90      95
116 Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
117      100      105      110
120 Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
121      115      120      125
124 Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
125      130      135      140
128 Glu Gln Phe Glu Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
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132 Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
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136 <210> SEQ ID NO: 3
137 <211> LENGTH: 519
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Synthetic DNA
145 <220> FEATURE:
146 <221> NAME/KEY: CDS

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147 <222> LOCATION: (1)..(519)

149 <400> SEQUENCE: 3

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150 atg gct aat tct gac gtc acc cgc cac atc ctg tcc gta ctc gtt cag      48
151 Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
152 1          5          10          15
154 gac gta gac ggt gac ttt tcc cgc gta tca ggt atg ttc acc cga cgc      96
155 Asp Val Asp Gly Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg
156          20          25          30
158 gca ttc aac ctc gtg tcc ctc gtg tct gca aag acc gaa aca cac ggc      144
159 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
160          35          40          45
162 atc aac cgc atc acg gtt gtt gtc gac gcc gac gag ctc aac att gag      192
163 Ile Asn Arg Ile Thr Val Val Asp Ala Asp Glu Leu Asn Ile Glu
164          50          55          60
166 cag atc acc aag cag ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg      240
167 Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
168 65          70          75          80
170 cga ctt gat gaa gag acc act atc gcc cgc gca atc atg ctg gtt aag      288
171 Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
172          85          90          95
174 gtc tct gcg gac agc acc aac cgt ccg cag atc gtc gac gcc gcg aac      336
175 Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
176          100          105          110
178 atc ttc cgc gcc cga gtc gtc gac gtg gct cca gac tct gtg gtt att      384
179 Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
180          115          120          125
182 gaa tcc aca ggc acc cca ggc aag ctc cgc gca ctg ctt gac gtg atg      432
183 Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
184          130          135          140
186 gaa cca tcc gga atc gcg gaa ctg atc caa tcc gga cag att gca ctc      480
187 Glu Pro Ser Gly Ile Ala Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
188 145          150          155          160
190 aac cgc ggt ccg aag acc atg gct ccg gcc aag atc taa      519
191 Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
192          165          170

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195 <210> SEQ ID NO: 4

196 <211> LENGTH: 172

197 <212> TYPE: PRT

198 <213> ORGANISM: Artificial Sequence

200 <220> FEATURE:

201 <223> OTHER INFORMATION: Synthetic Construct

203 <400> SEQUENCE: 4

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209 Asp Val Asp Gly Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg
210          20          25          30
213 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
214          35          40          45
217 Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu

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218      50      55      60
221 Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
222 65      70      75      80
225 Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
226      85      90      95
229 Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
230      100      105      110
233 Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
234      115      120      125
237 Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
238      130      135      140
241 Glu Pro Ser Gly Ile Ala Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
242 145      150      155      160
245 Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
246      165      170
249 <210> SEQ ID NO: 5
250 <211> LENGTH: 17
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Synthetic DNA
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262 <211> LENGTH: 22
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Synthetic DNA
269 <400> SEQUENCE: 6
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273 <210> SEQ ID NO: 7
274 <211> LENGTH: 26
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Synthetic DNA
281 <400> SEQUENCE: 7
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285 <210> SEQ ID NO: 8
286 <211> LENGTH: 19
287 <212> TYPE: DNA
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Synthetic DNA
293 <400> SEQUENCE: 8
294 gtttagaact tggccggag
297 <210> SEQ ID NO: 9
298 <211> LENGTH: 20

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299 <212> TYPE: DNA
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303 <223> OTHER INFORMATION: Synthetic DNA
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317 1 5 10 15
320 Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg
321 20 25 30
324 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
325 35 40 45
328 Ile Asn Arg Ile Thr Val Val Val Asp
329 50 55
332 <210> SEQ ID NO: 11
333 <211> LENGTH: 53
334 <212> TYPE: PRT
335 <213> ORGANISM: S. cinnamonensis
337 <400> SEQUENCE: 11
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340 1 5 10 15
343 Val Leu Ala Arg Ile Thr Ala Leu Phe Ser Arg Arg Gly Phe Asn Ile
344 20 25 30
347 Asp Ser Leu Ala Val Gly Val Thr Glu His Pro Asp Ile Ser Arg Ile
348 35 40 45
351 Thr Ile Val Val Asn
352 50
355 <210> SEQ ID NO: 12
356 <211> LENGTH: 57
357 <212> TYPE: PRT
358 <213> ORGANISM: Escherichia Coli
360 <400> SEQUENCE: 12
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366 Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg
367 20 25 30
370 Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp
371 35 40 45
374 Lys Ser His Ile Trp Leu Leu Val Asn
375 50 55

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VERIFICATION SUMMARY

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